Please amend the specification by deleting the description of Figure 5 on page 5, lines 5–8 and replacing with the text shown below:

Figure 5 shows colonies of Hela and HF cells formed after transfecting cells with vector control (5A and 5B), with HTS1 (hPPAN) (5C and 5D), and with a frameshift mutant (FS) (5E and 5F), followed by two weeks of hygromycin selection.

Please amend the specification by deleting the description page 9 lines 14-27 and replacing with the text shown below:

In general, a nucleic acid molecule that has "substantially the same nucleotide sequence" as a reference sequence will have greater than about 60% identity, such as greater than about 65%, 70%, 75% identity with the reference sequence, such as greater than about 80%, 85%, 90%, 95%, 97% or 99% identity to the reference sequence over the length of the two sequences being compared. Identity of any two nucleic acid sequences can be determined by those skilled in the art based, for example, on a BLAST 2.0 computer alignment, using default parameters. BLAST 2.0 searching is available as described by Tatiana et al., <u>FEMS Microbiol Lett.</u> 174.247-250 (1999). The BLAST program is available online at U.S. National Cancer Institute's National Cancer Biotechnology Information ("NCBI") website.

Please amend the specification by deleting the description page 19 lines 16-28 and replacing with the text shown below:

A tumor suppressor nucleic acid molecule containing at least fifteen contiguous nucleotides of SEQ ID NO:2, or a functional fragment thereof, does not consist of a nucleotide sequence having the exact endpoints of nucleotide sequences deposited in public databases at the time of filing, such as Expressed Sequence Tags (ESTs), Sequence Tagged Sites (STSs) and genomic fragments, deposited in databases such as the nr, dbest, dbsts, gss and htgs databases, which are available for searching using the program BLASTN 2.0.9 [May-07-1999] described by Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997). The BLAST program is available online at U.S. National Cancer Institute's

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